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CGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAA
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TCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGGGG
CTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCG
GGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGT
CTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTC
TGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCCG
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CCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCT
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AGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCC
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CGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCT
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GCCGACTGATGCCTTCTGAACAATGGAAAGGCATTATTGCCGTAAGCCGT
GGCGGTCTGGTACCGGTGGGTGAAGACCAGAAACAGCACCTCGATCTGAG
CCGCGATATTGCCCAGCGTTTCAACGCGCTGTATGGCGAGATCGATCCCG
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GGCCTTGGAGGACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGC

Figure 1

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TGCACGGTTACGATGCGCCCATCTACACCAACGTGACCTATCCCATTACG
GTCAATCCGCCGTTTGTTCCCACGGAGAATCCGACGGGTTGTTACTCGCT
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ATTTTTGATGGCGTTAACTCGGCGTTTCATCTGTGGTGCAACGGGCGCTG
GGTCGGTTACGGCCAAGACAGTCGTTTGGCGTCTTAATTTGAGCTCGAGC
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AGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAA
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GAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATAT
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TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA
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Figure 1

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CGGCCGGCCGCAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGAC
AGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATT
TCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATAC
GGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCA
CGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGC
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Figure 1

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CCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTG
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CCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGAC

Figure 2

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Figure 2

```
          •       20        •       40        •       60        •       80
   1 AAGGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA 80
     | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   1 ATGGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA 80
          •       20        •       40        •       60        •       80
          •      100        •      120        •      140        •      160
  81 CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGC 160
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  81 CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGC 160
          •      100        •      120        •      140        •      160
          •      180        •      200        •      220        •      240
 161 GAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGAC 240
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 161 GAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGAC 240
          •      180        •      200        •      220        •      240
          •      260        •      280        •      300        •      320
 241 CAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCC 320
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 241 CAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCC 320
          •      260        •      280        •      300        •      320
          •      340        •      360        •      380        •      400
 321 TCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATC 400
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 321 TCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATC 400
          •      340        •      360        •      380        •      400
          •      420        •      440        •      460        •      480
 401 CAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTC 480
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 401 CAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTC 480
          •      420        •      440        •      460        •      480
          •      500        •      520        •      540        •      560
 481 CCTGACCCTGACAAGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGA 560
     ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 481 CCTGACCCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGA 560
          •      500        •      520        •      540        •      560
          •      580        •      600        •      620        •      640
 561 AGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGACCGGTGGTACCTCACCCTTACCGAGTCGGCGACA 640
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 561 AGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGACCGGTGGTACCTCACCCTTACCGAGTCGGCGACA 640
          •      580        •      600        •      620        •      640
          •      660        •      680        •      700        •      720
 641 CAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCC 720
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 641 CAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCC 720
          •      660        •      680        •      700        •      720
          •      740        •      760        •      780        •      800
 721 ACCGCCCTCAAAGTAGACGGCATCGCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATC 800
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 721 ACCGCCCTCAAAGTAGACGGCATCGCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATC 800
          •      740        •      760        •      780        •      800
          •      820
 801 CTCTAGACTGCCGGATCCCAGTGTGG (SEQ ID NO:2)                                         826
     ||||||||||||||||||||||||||
 801 CTCTAGACTGCCGGATCCCAGTGTGG (SEQ ID NO:1)                                         826
          •      820

% Identity =   99.8 (824/826)
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Figure 3

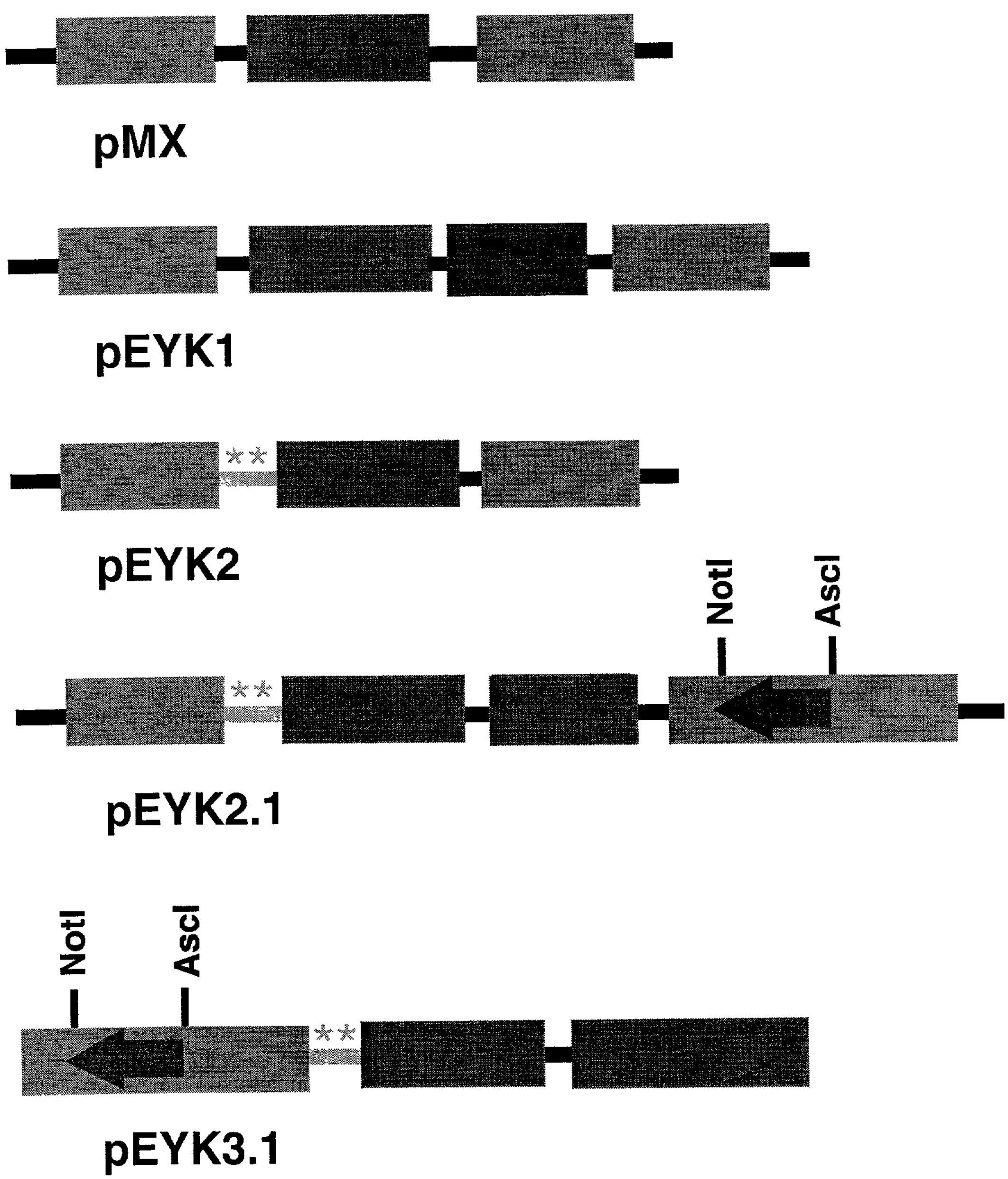
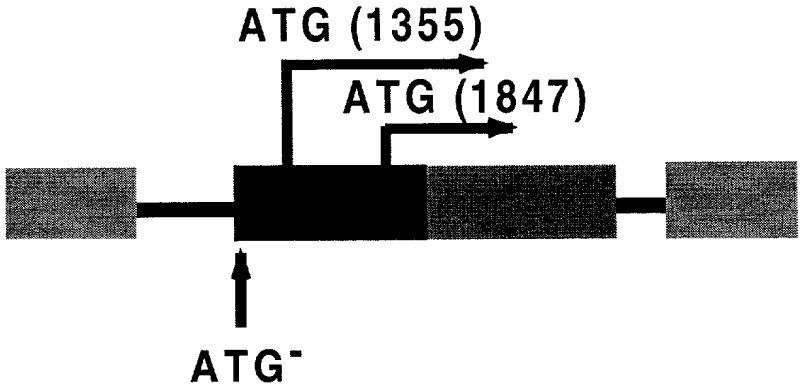


Figure 4

A) pMX



B) pEYK2

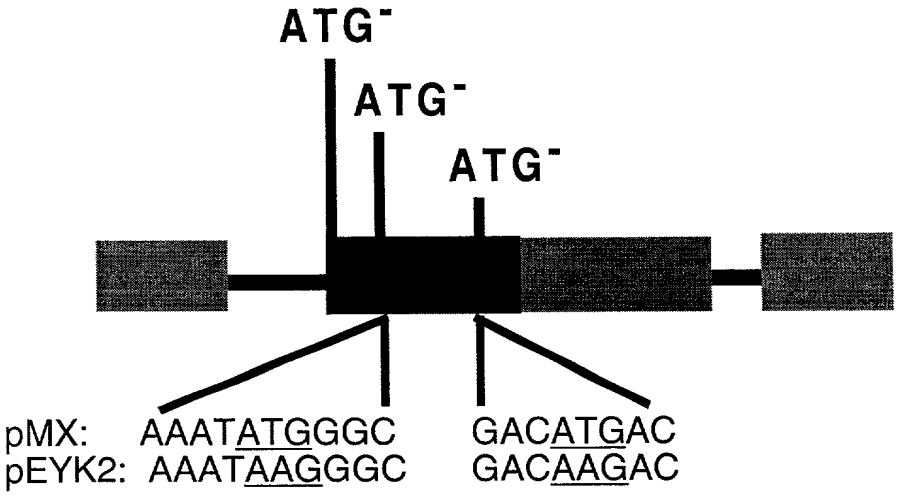


Figure 5

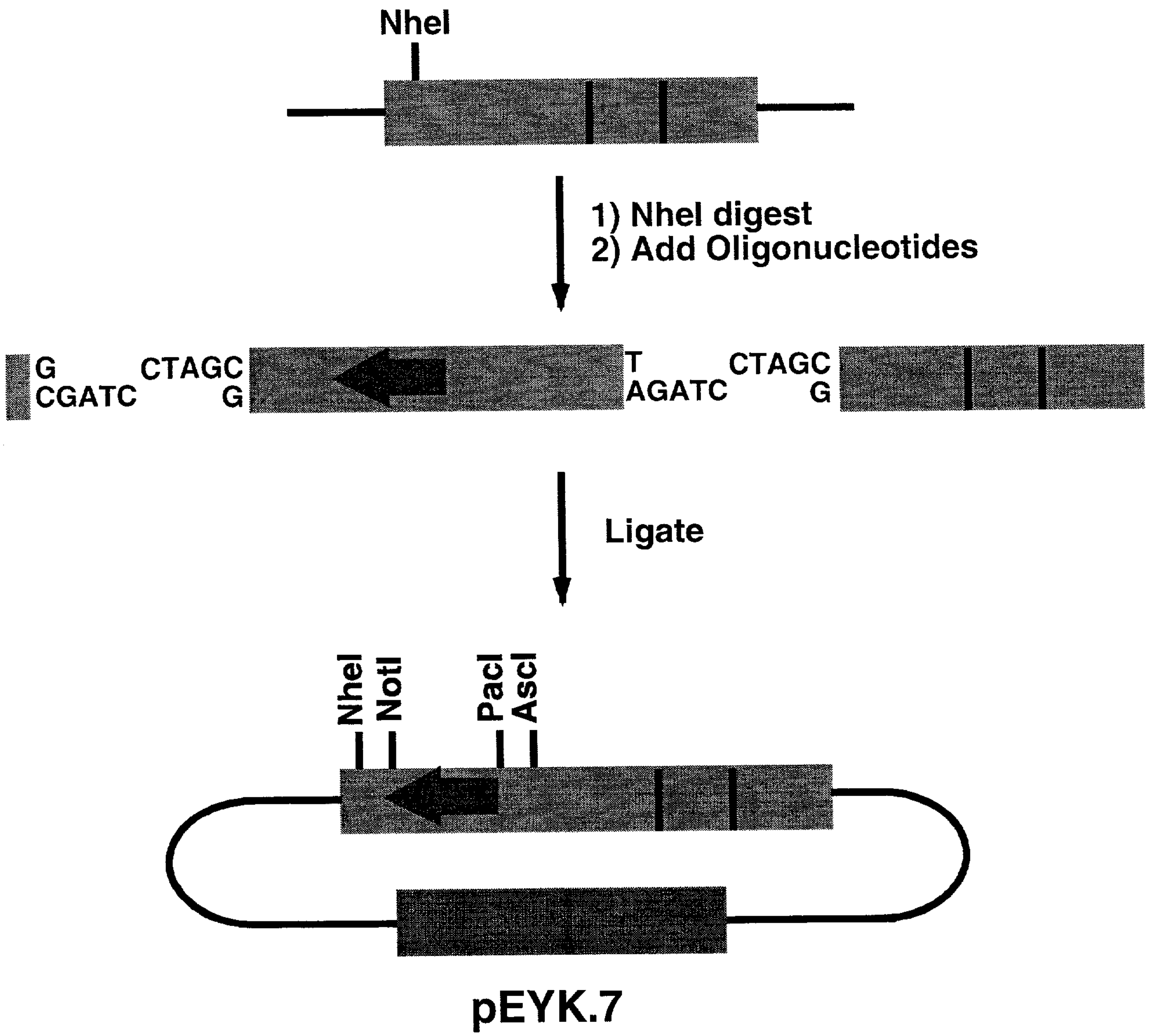

NheI
1) NheI digest
2) Add Oligonucleotides
G
CGATC
CTAGC
G
T
AGATC
CTAGC
G
Ligate
NheI
NotI
PacI
AscI
pEYK.7

Figure 6

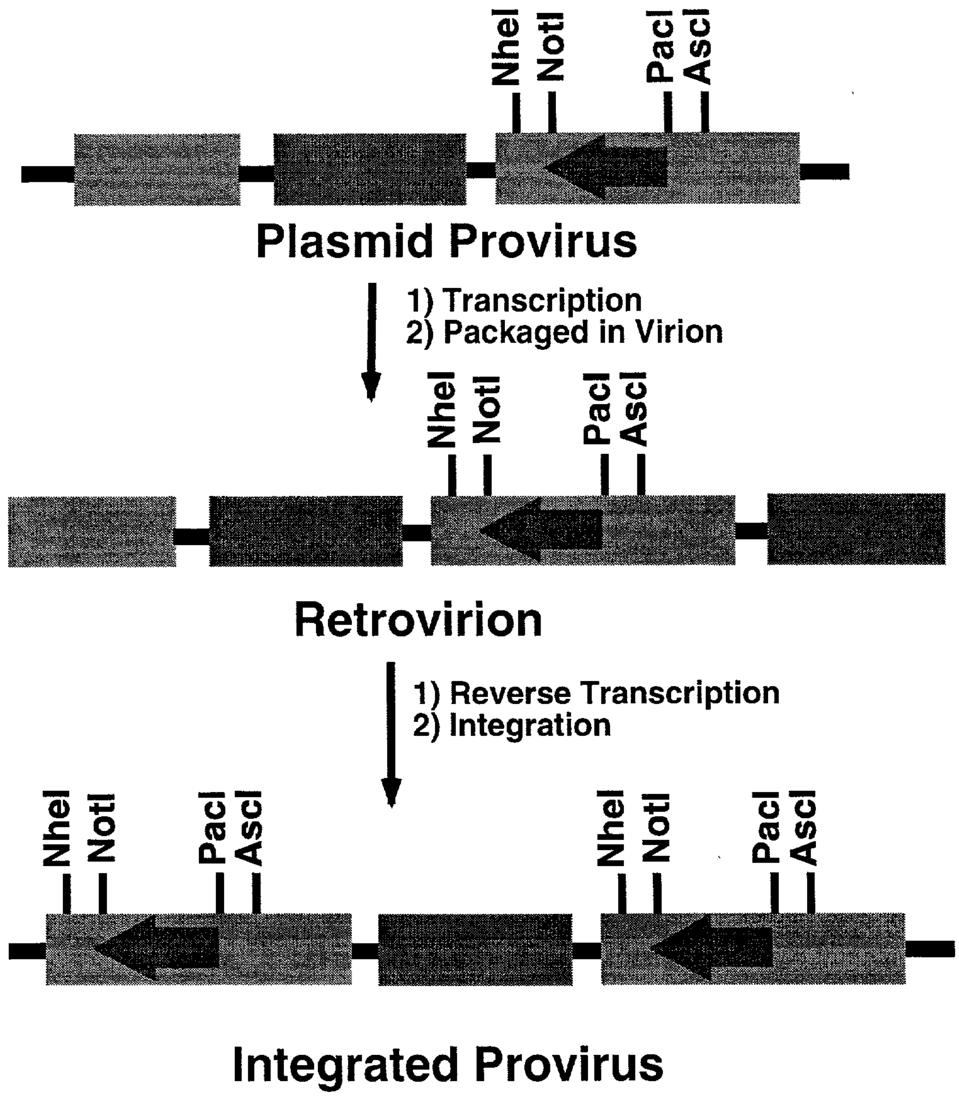

NheI
NotI
PacI
AscI
Plasmid Provirus
1) Transcription
2) Packaged in Virion
NheI
NotI
PacI
AscI
Retrovirion
1) Reverse Transcription
2) Integration
NheI
NotI
PacI
AscI
NheI
NotI
PacI
AscI
Integrated Provirus

Figure 7

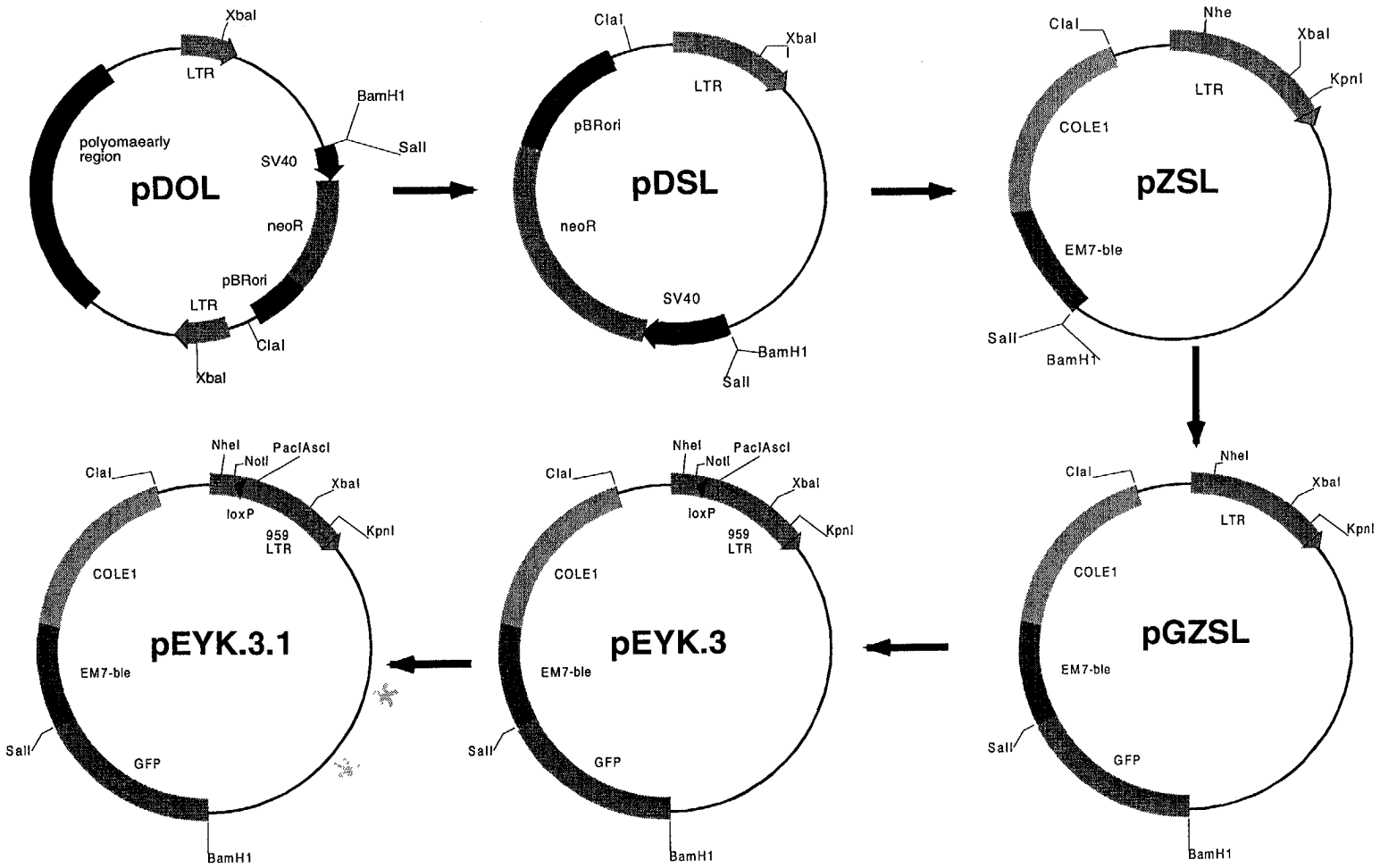
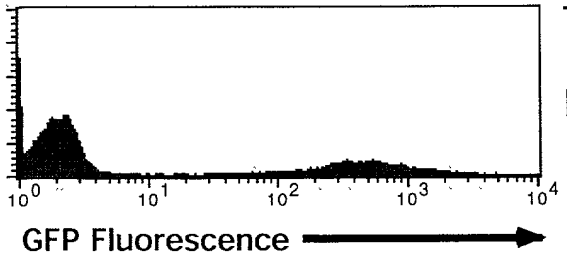

pDOL
XbaI
LTR
BamH1
SalI
polyomaearly region
SV40
neoR
pBRori
LTR
ClaI
XbaI
pDSL
ClaI
XbaI
LTR
pBRori
neoR
SV40
BamH1
SalI
pZSL
ClaI
NheI
XbaI
KpnI
LTR
COLE1
EM7-ble
SalI
BamH1
pGZSL
ClaI
NheI
XbaI
KpnI
LTR
COLE1
EM7-ble
SalI
GFP
BamH1
pEYK.3
ClaI
NheI
PacIAscI
NotI
XbaI
loxP
959 LTR
KpnI
COLE1
EM7-ble
SalI
GFP
BamH1
pEYK.3.1
ClaI
NheI
PacIAscI
NotI
XbaI
loxP
959 LTR
KpnI
COLE1
EM7-ble
SalI
GFP
BamH1

Figure 8

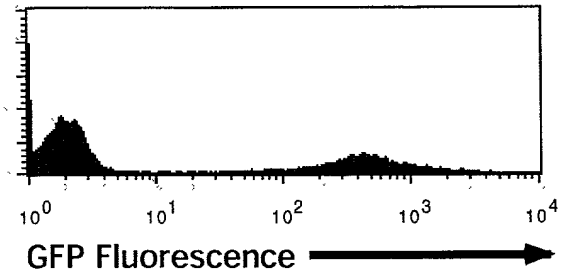
pEYK.2.2



Titer: 7.2×10^6 IFU / mL

Fold expression: 206

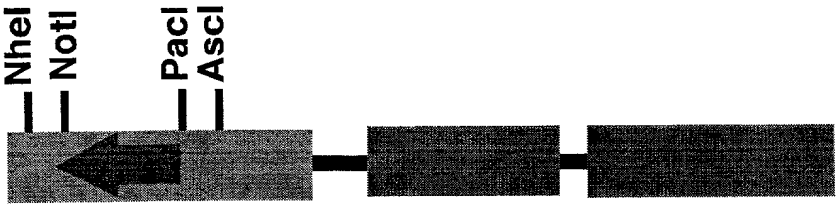
pEYK.2.3



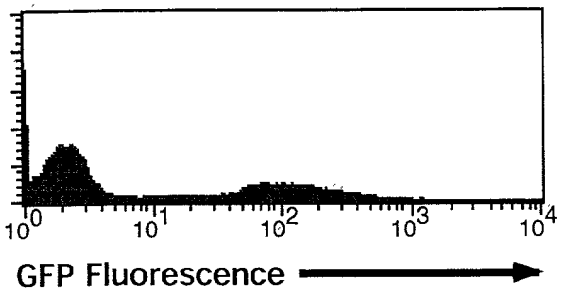
Titer: 7.0×10^6 IFU / mL

Fold expression: 203

Figure 9

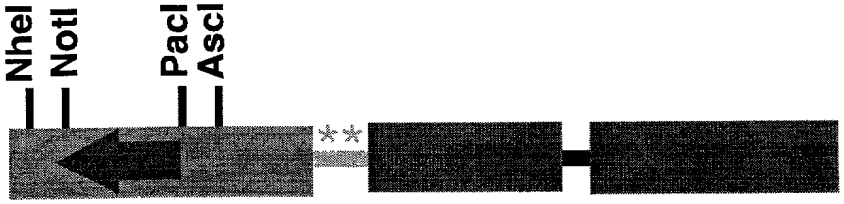


pEYK3

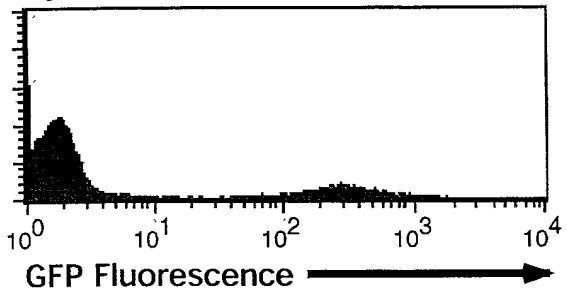


Titer: 1.0×10^6 IFU / mL

Fold expression: 33



pEYK3.1



Titer: 1.0×10^6 IFU / mL

Fold expression: 121

Figure 10

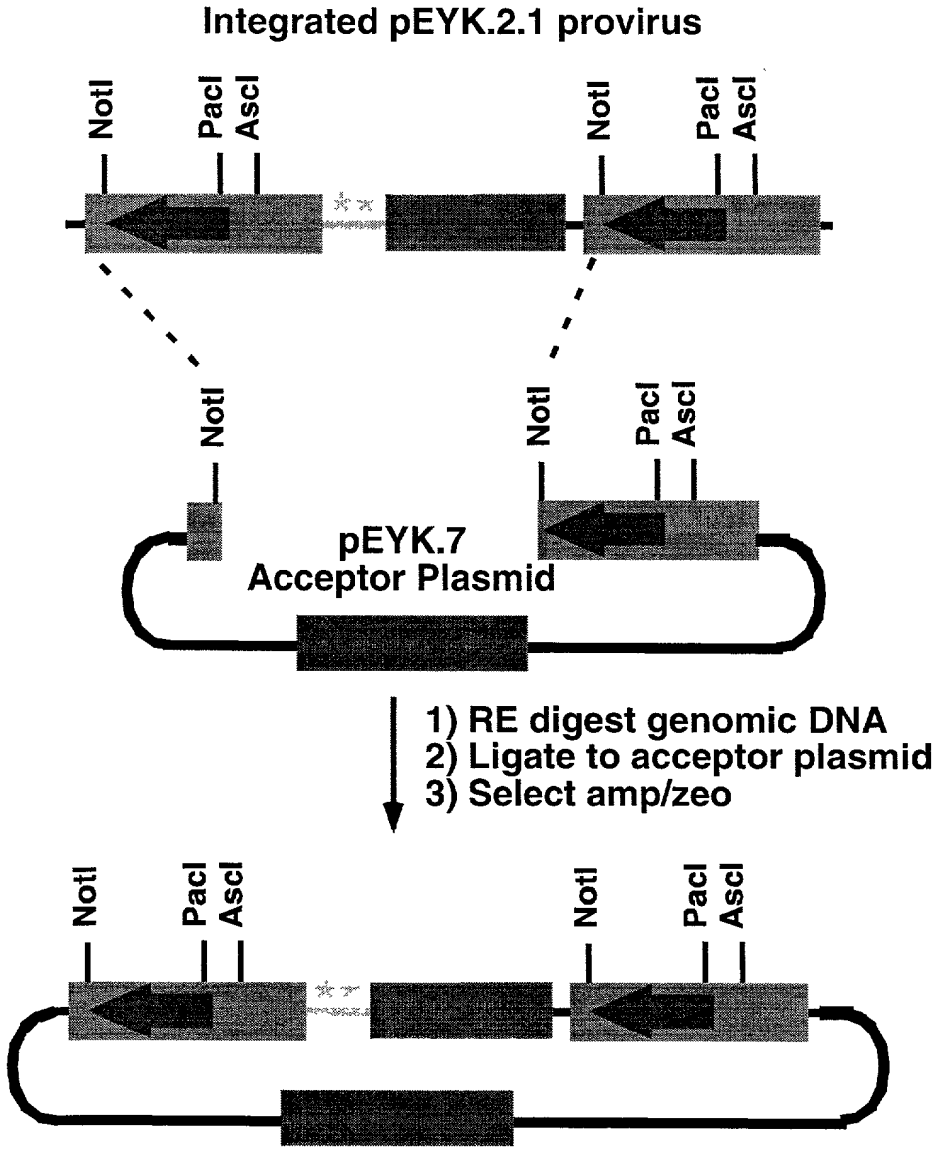


Figure 11

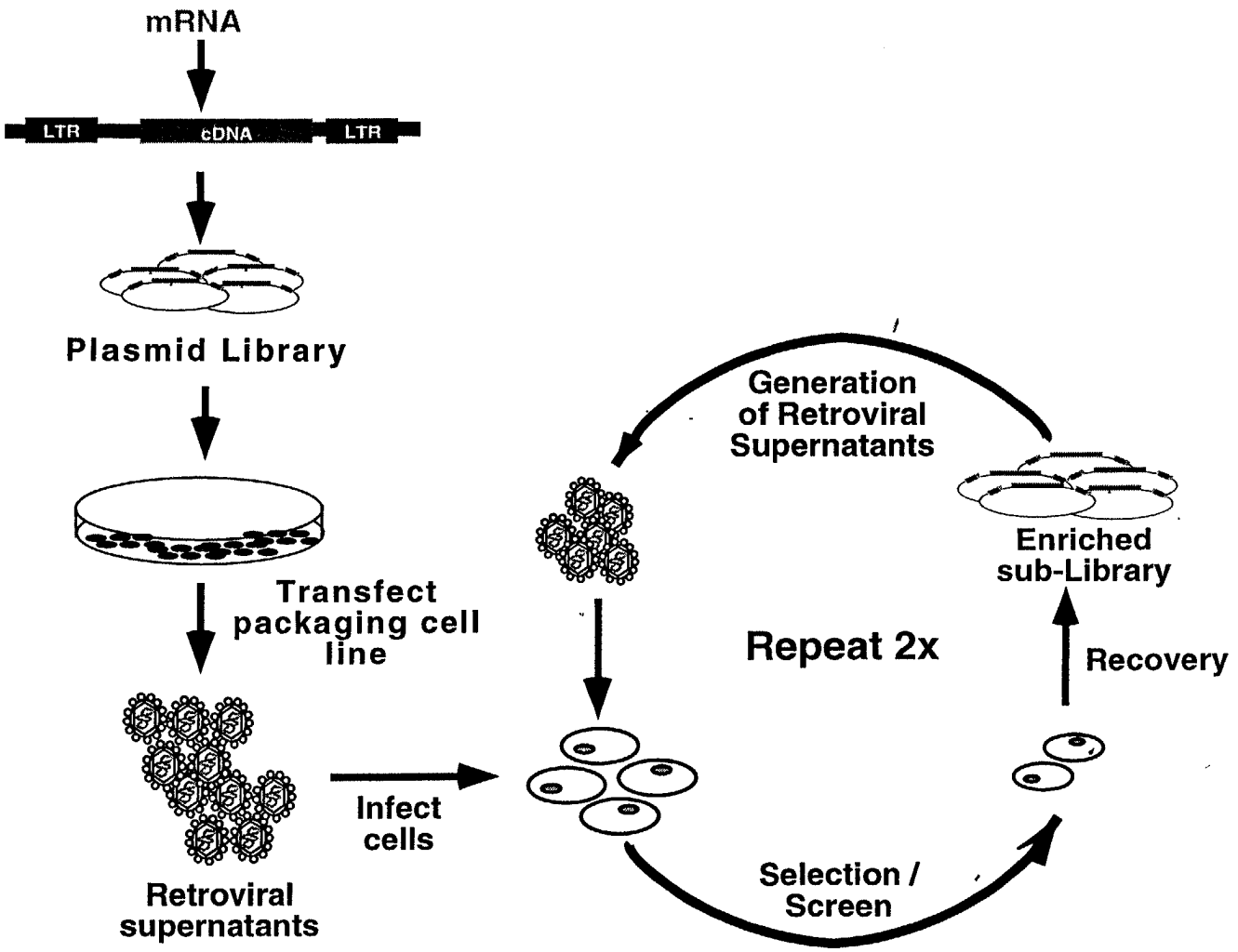
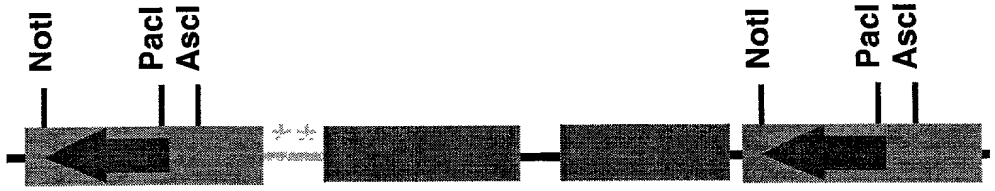


Figure 12

A) Integrated B/A-pEYK.3.1 provirus



B)

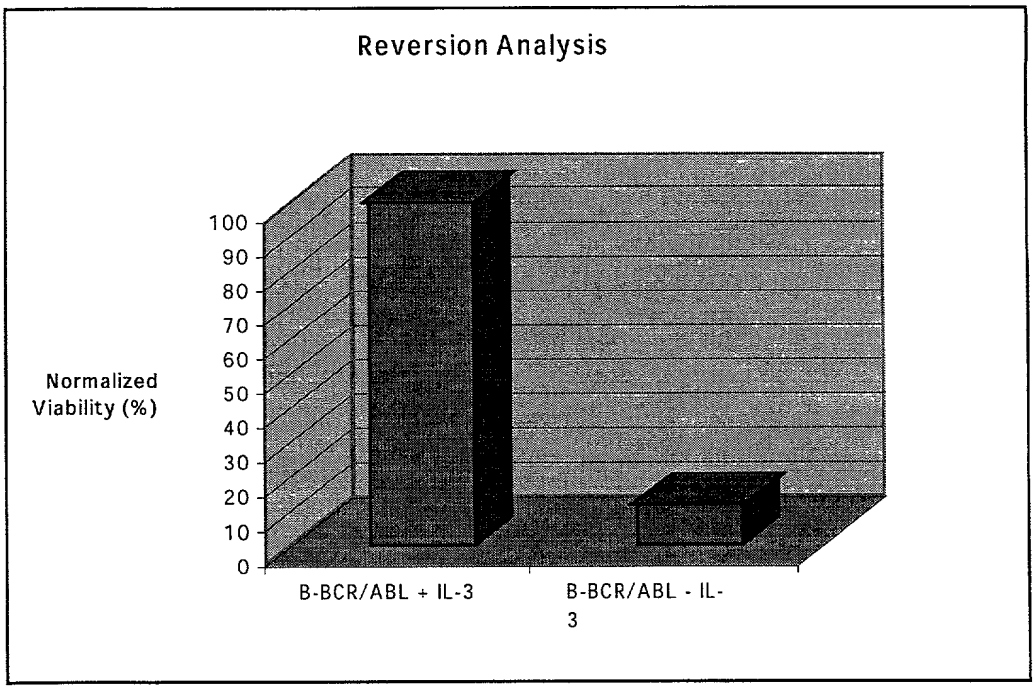


Figure 13